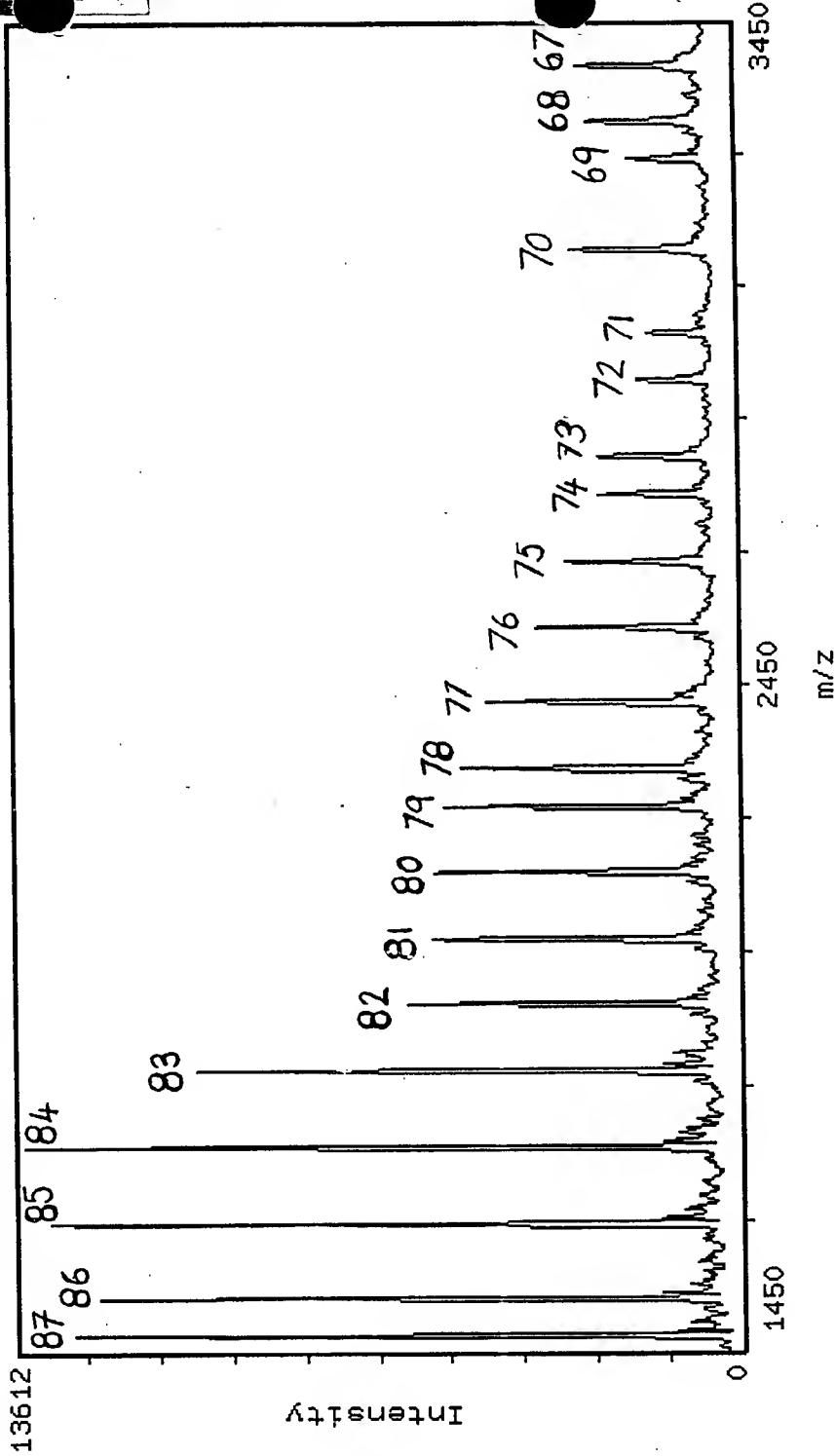


Figure A

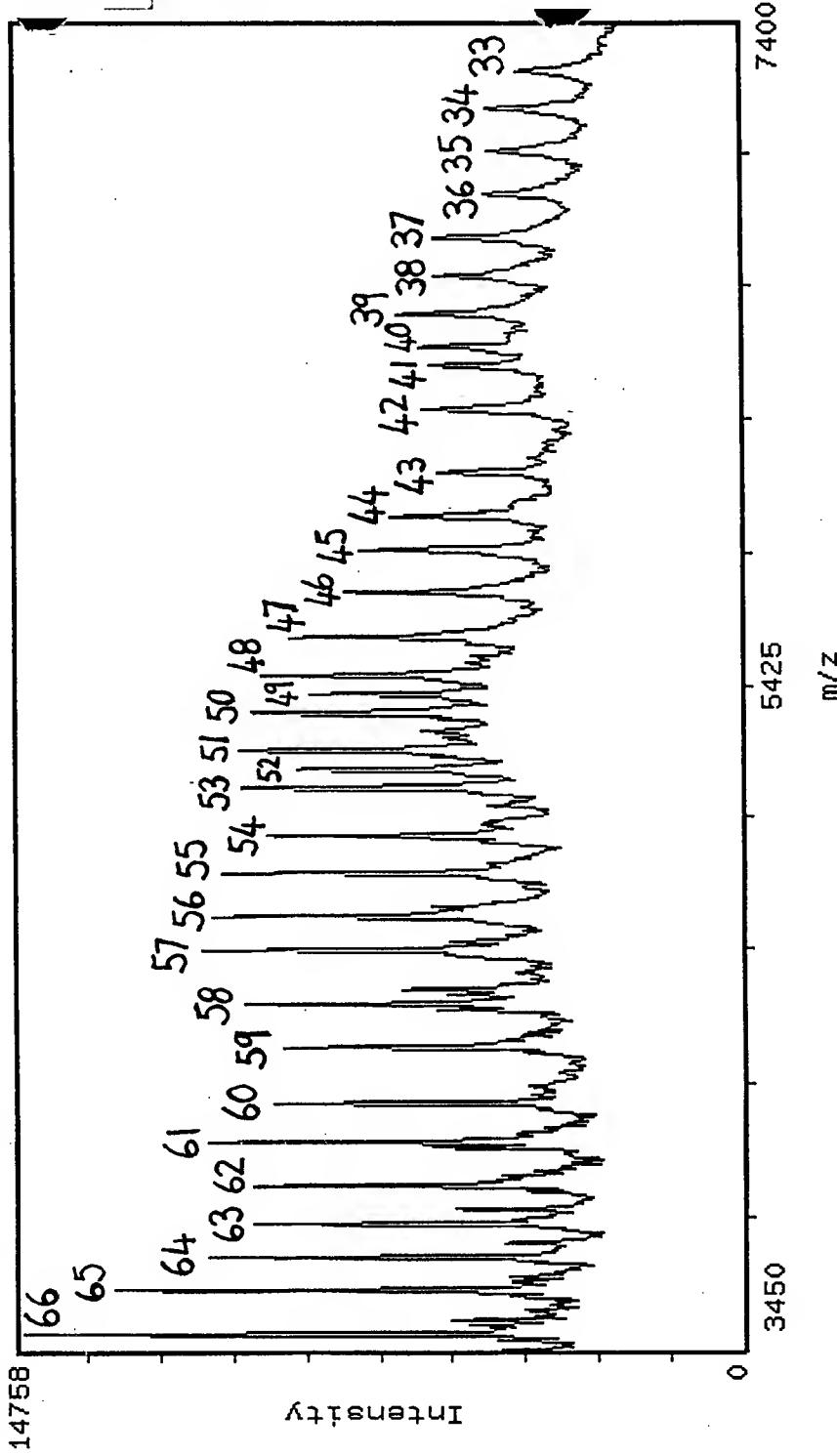
HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=99,67)



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FIGURE B

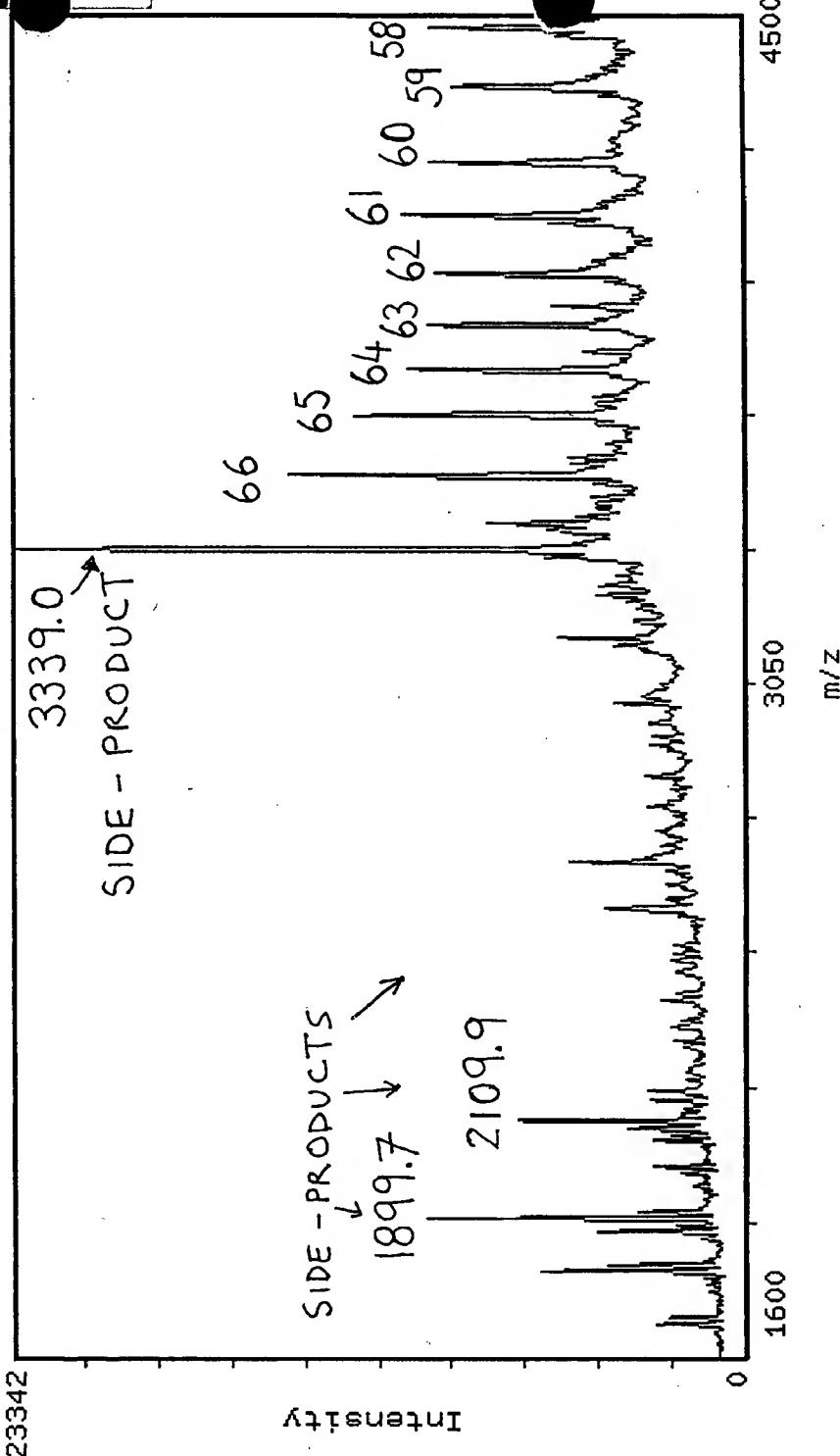
HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=66,33)



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FIGURE C

LOW MASS REGION OF HIV-1 PROTEASE
PEPTIDE LADDER (99-N, WHERE N=66,33)



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IDENTIFICATION OF SIDE-REACTION PRODUCT

MEASURED MM OF MAJOR SIDE-PRODUCT = 3339.0

CALCULATED MM OF PEPTIDE (99-69) = 3242.9

DIFFERENCE = 96.1

HIS-69 APPEARS TO BE TRIFLUOROACETYLATED

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1-2-3-4-5-6-7-8-9.....-n-(OH) INTACT STARTING
PEPTIDE CHAIN

(X)-1-2-3-4-5-6-7-8-9.....-n-(OH)

(X)-2-3-4-5-6-7-8-9.....-n-(OH)

(X)-3-4-5-6-7-8-9.....-n-(OH)

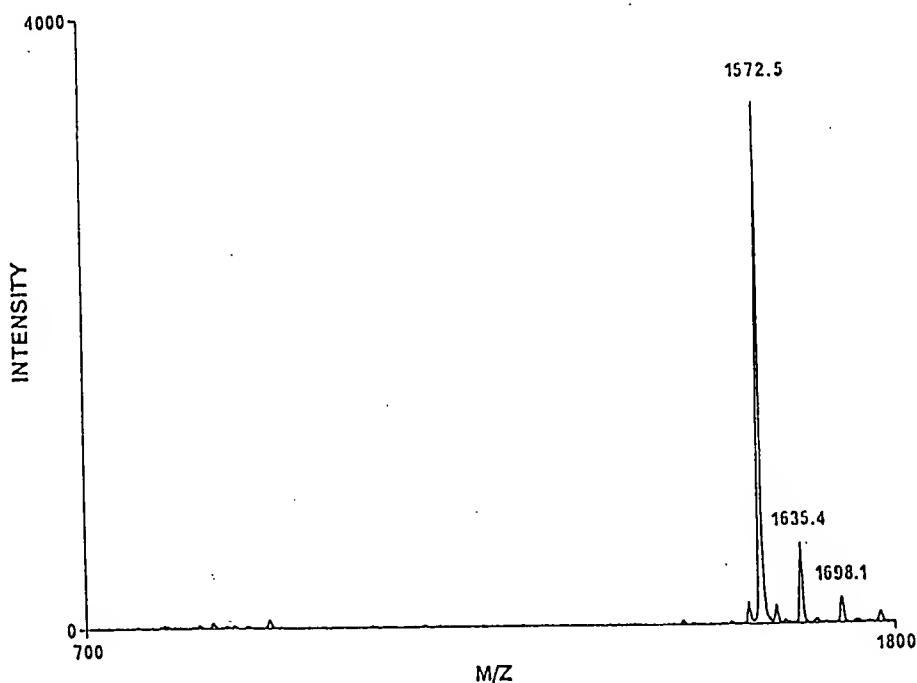
(X)-4-5-6-7-8-9.....-n-(OH)

(X)-5-6-7-8-9.....-n-(OH)

(Figure 1)

etc.

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*
Figure 1. Positive ion matrix-assisted laser desorption mass spectrum of [Glu¹]-Fibrinopeptide B.

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21.

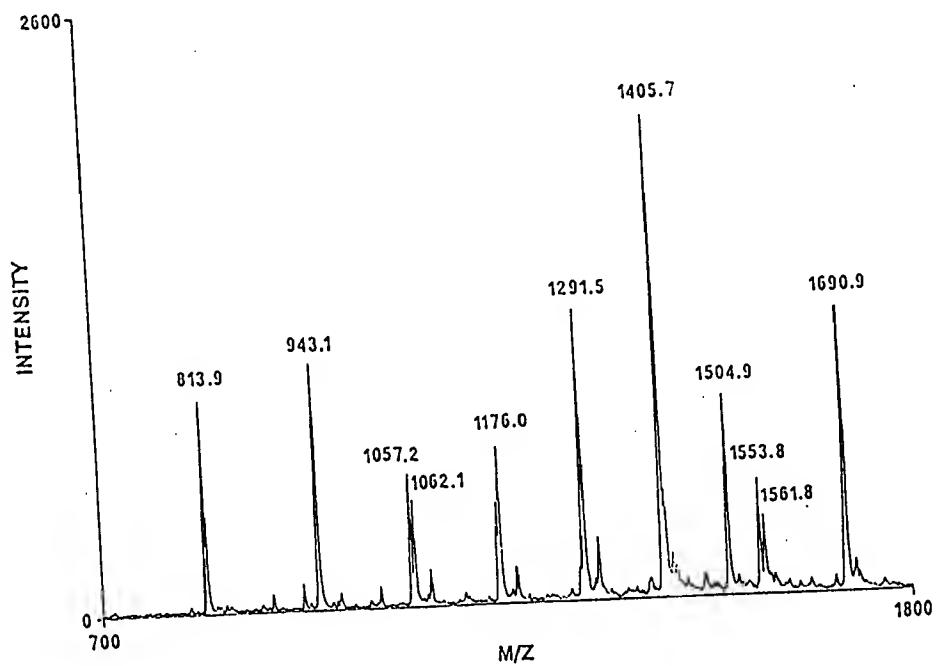
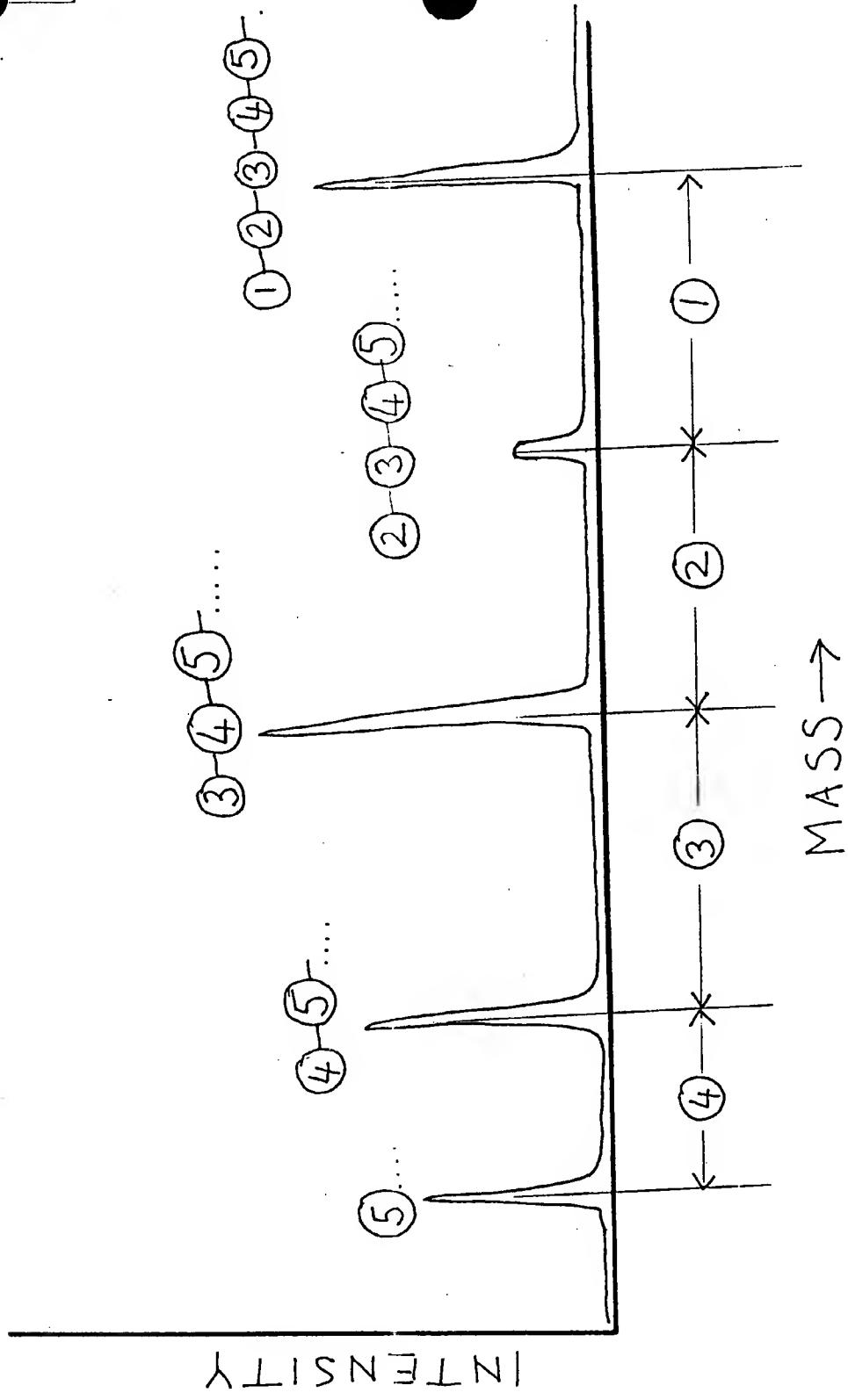
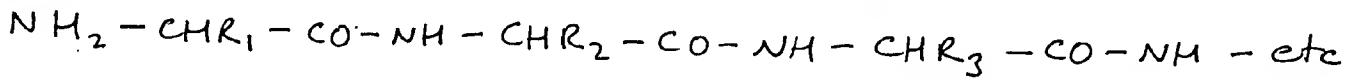


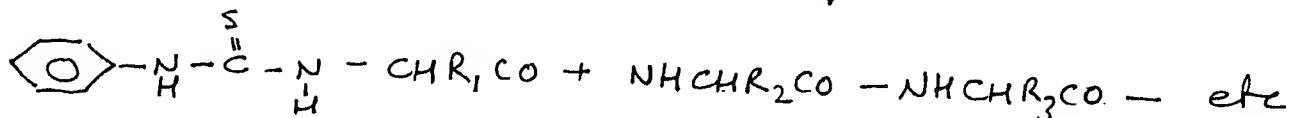
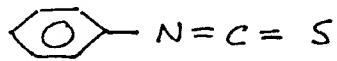
Figure 2.* Positive ion matrix-assisted laser desorption mass spectrum of [Glu¹]-Fibrinopeptide B after 7 cycles of modified Edman degradation.

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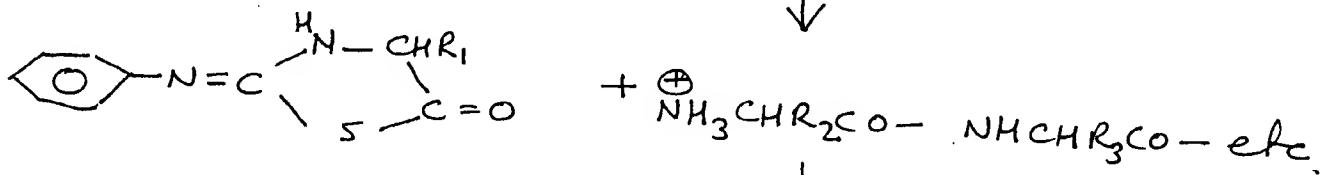


① Coupling : PITC in the presence
of base.



② Wash, dry.

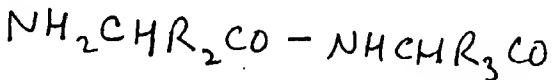
③ Cleavage : anhydrous acid



④ Wash (removes ATZ/PTH derivative)

⑤ Neutralize : base

⑥ Wash



Repeat steps 1 — 6

Figure 4 891177 15

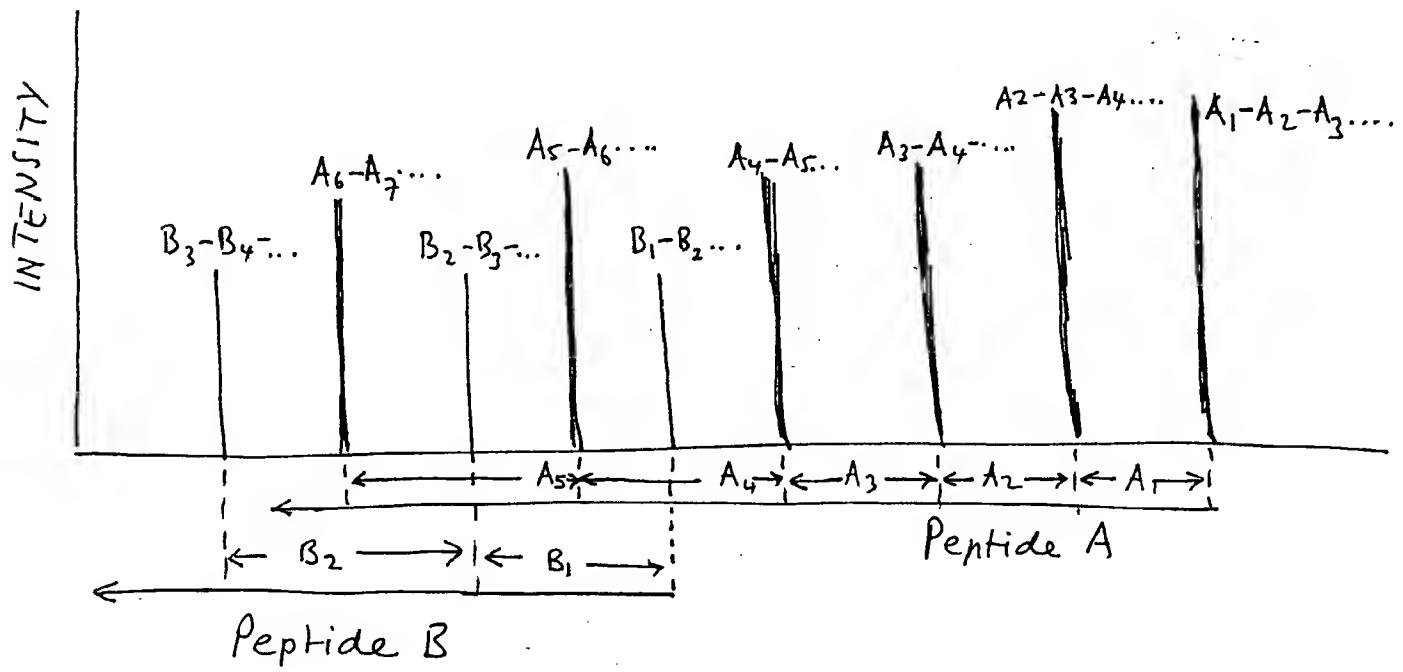
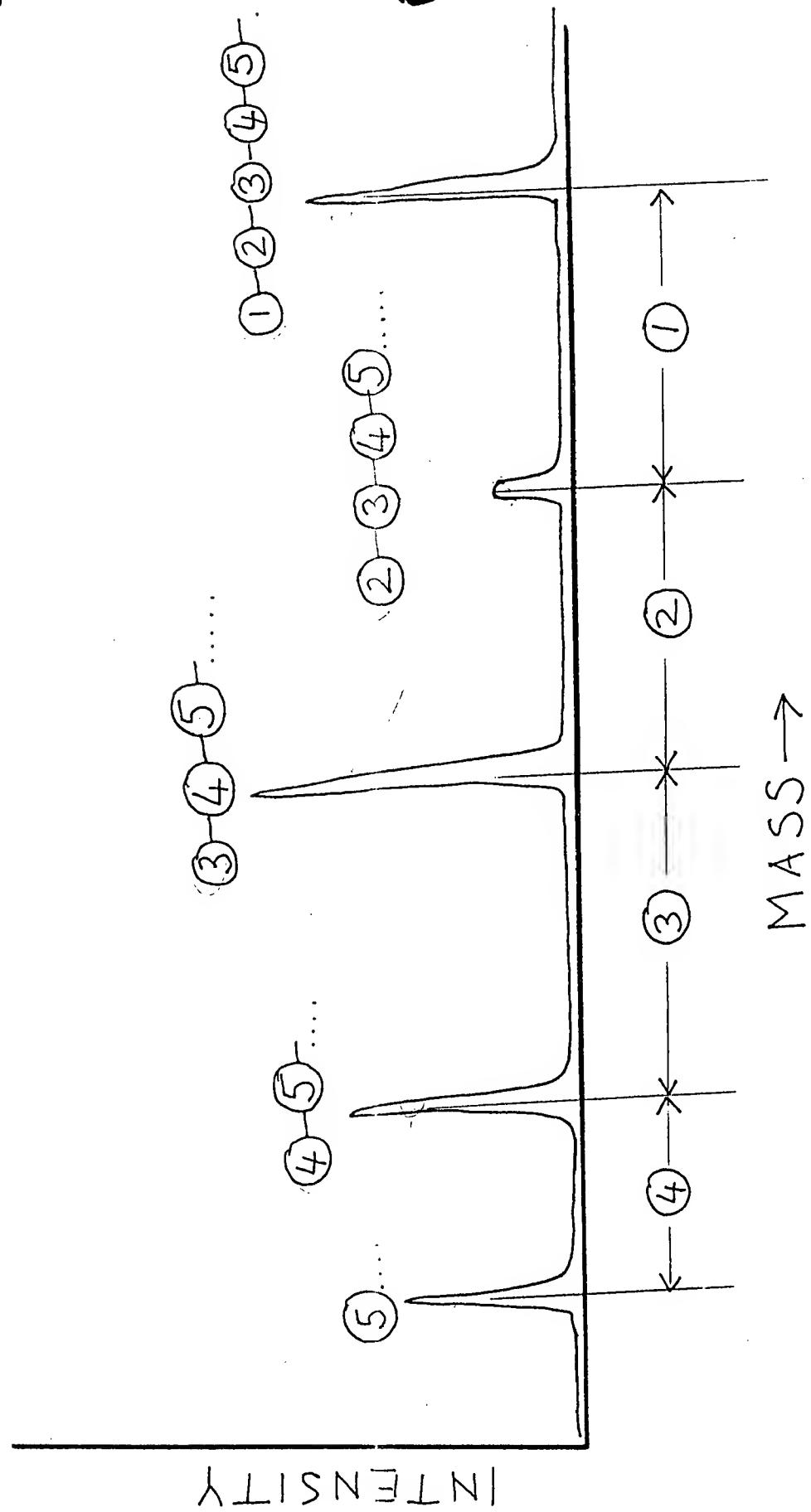
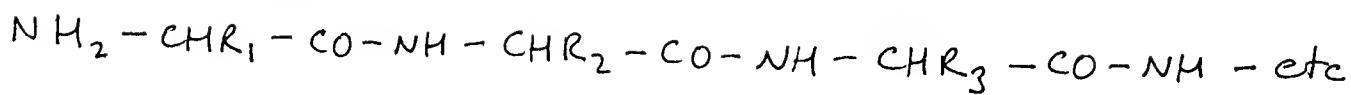


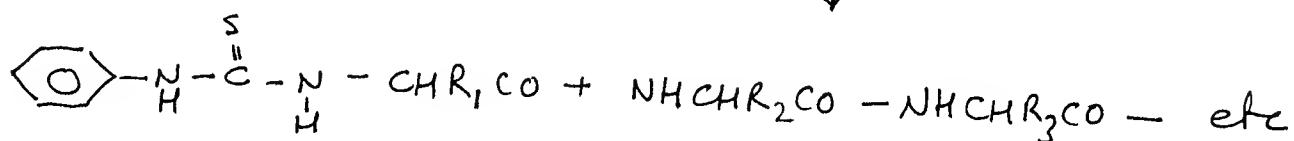
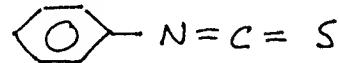
Figure 2

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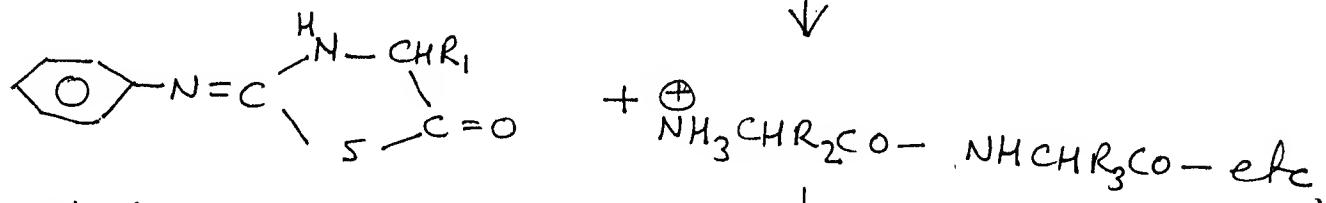


① Coupling : PITC in the presence of base.



② Wash, dry.

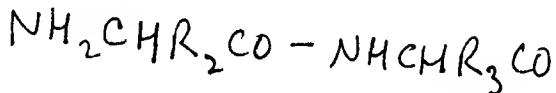
③ Cleavage : anhydrous acid



④ Wash (removes ATZ/PTH derivative)

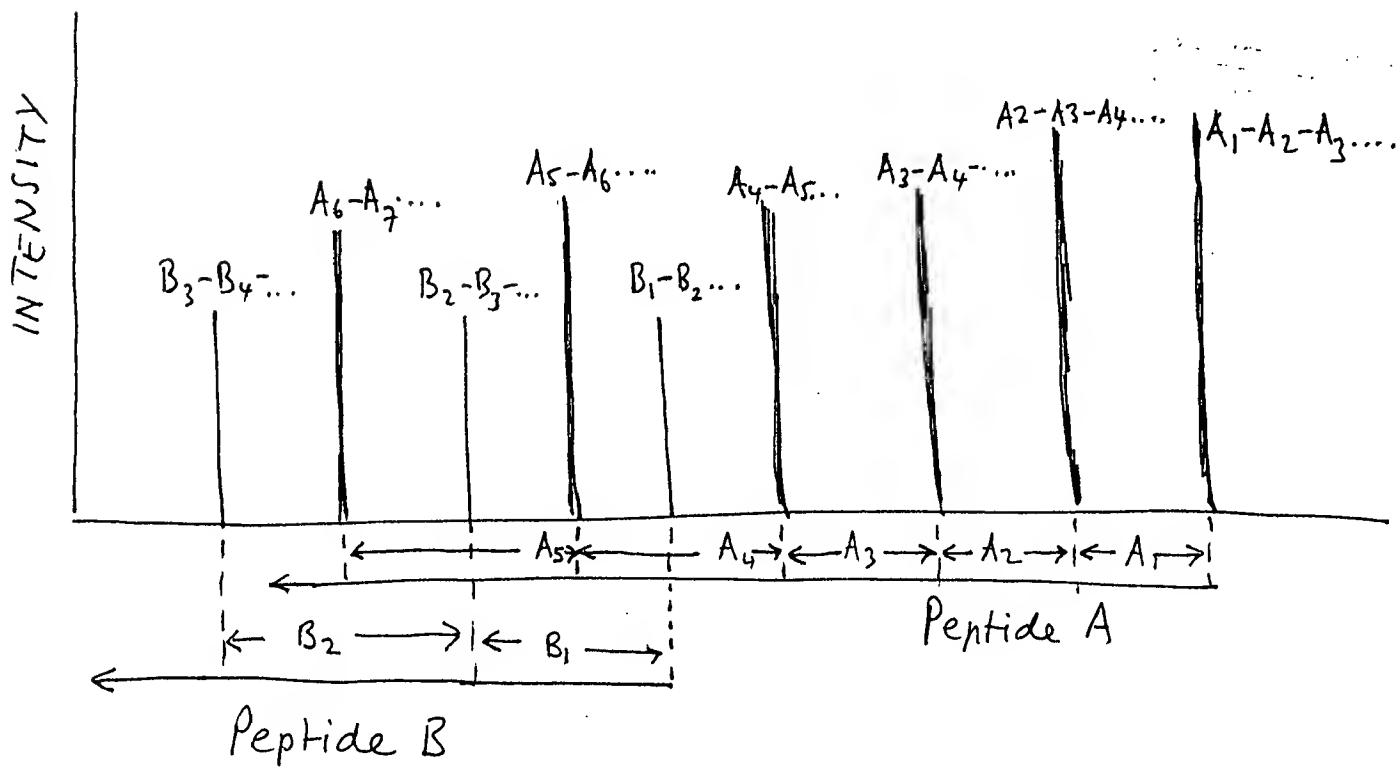
⑤ Neutralize : base

⑥ Wash



Repeat steps 1 - 6

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Figure A

HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=99,67)

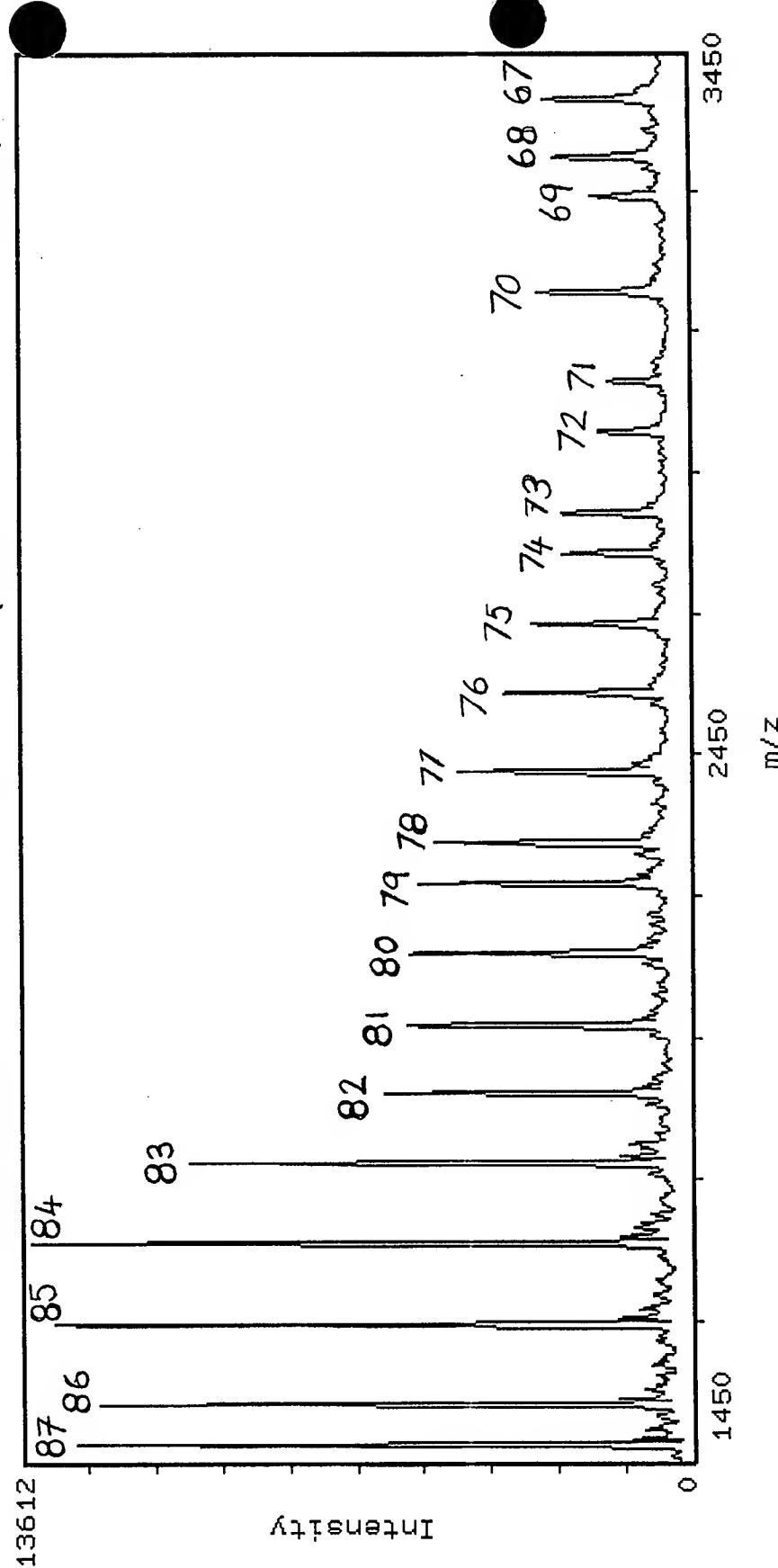
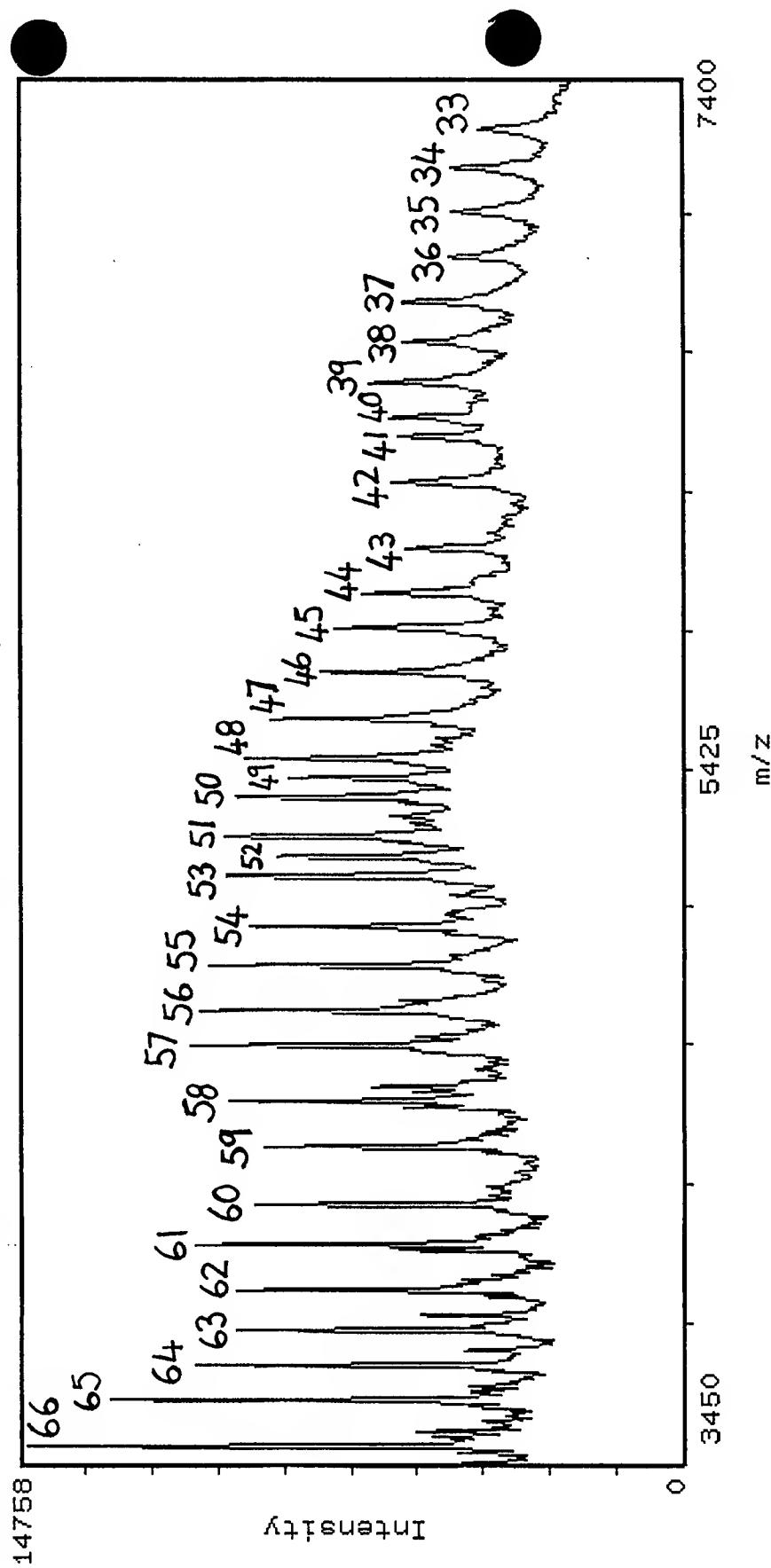


FIGURE B

HIV-1 PROTEASE PEPTIDE LADDER (99-N, WHERE N=66,33)

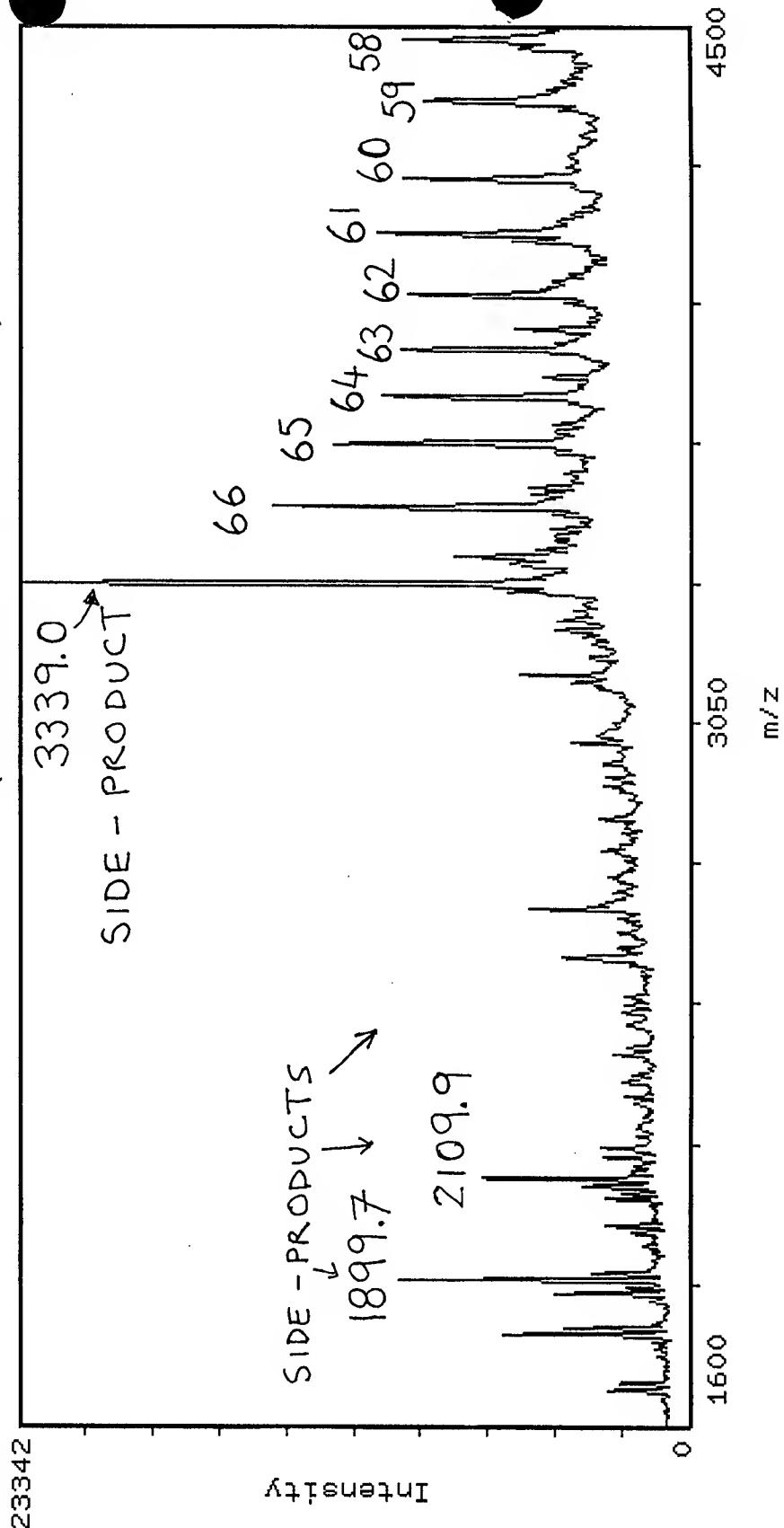


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FIGURE C

LOW MASS REGION OF HIV-1 PROTEASE
PEPTIDE LADDER (99-N, WHERE N=66,33)



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